Amendments to the Specification

Please delete the first paragraph on page 14 and replace it with the following amended paragraph.

Homology is measured by means well known in the art. For example % homology can be determined by any standard algorithm used to compare homologies. These include, but are not limited to BLAST 2.0 such as BLAST 2.0.4 and i. 2.0.5 available from the NIH ~~(See www.ncbi.nlm.nkh.gov/BLAST/newblast.html)~~ (Altschul, S.F., et al. Nucleic Acids Res. 25: 3389-3402 (1997)) and DNASIS (Hitachi Software Engineering America, Ltd.). These programs should preferably be set to an automatic setting such as the standard default setting for homology comparisons. As explained by the NIH, the scoring of gapped results tends to be more biologically meaningful than ungapped results.